

Fig. 1

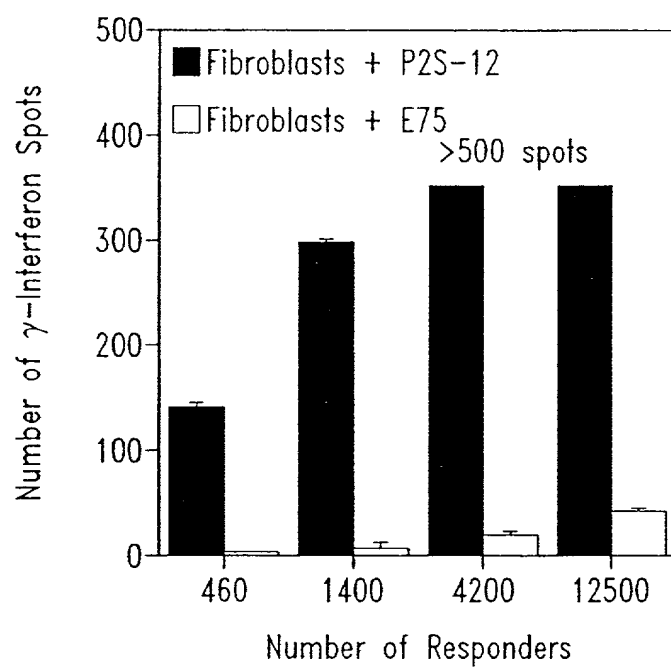


Fig. 2A

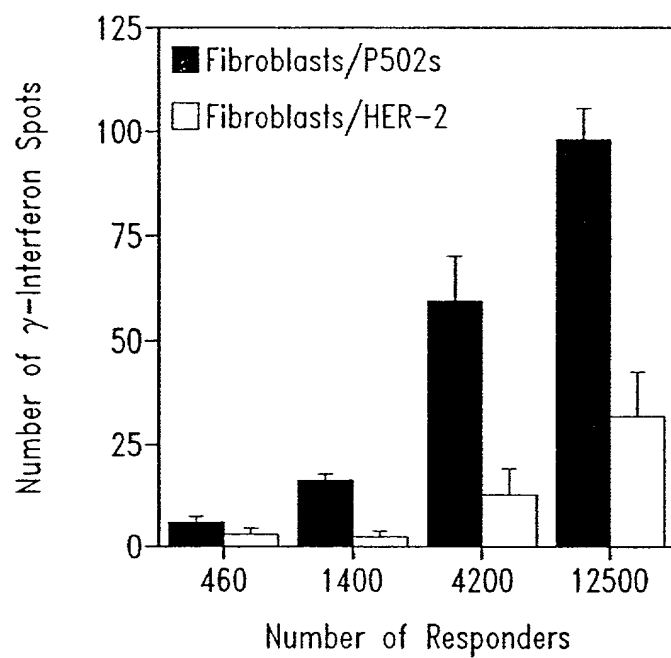


Fig. 2B

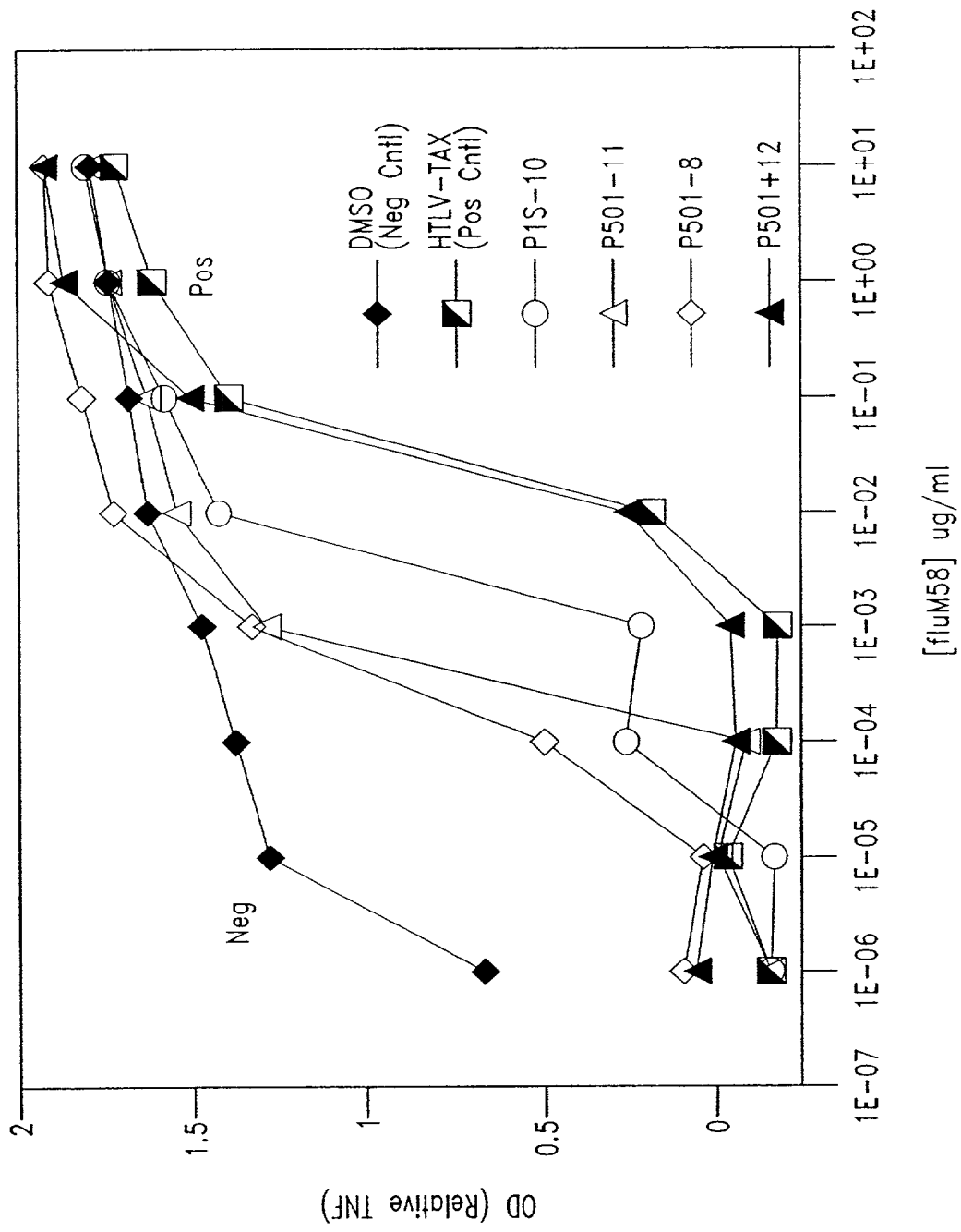


Fig. 3

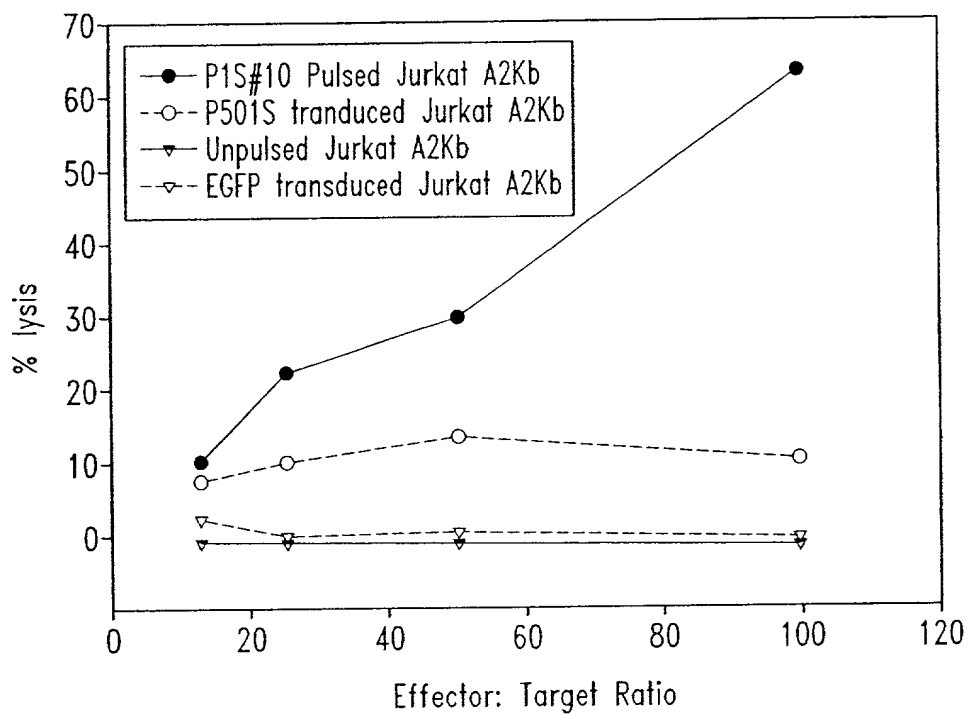


Fig. 4

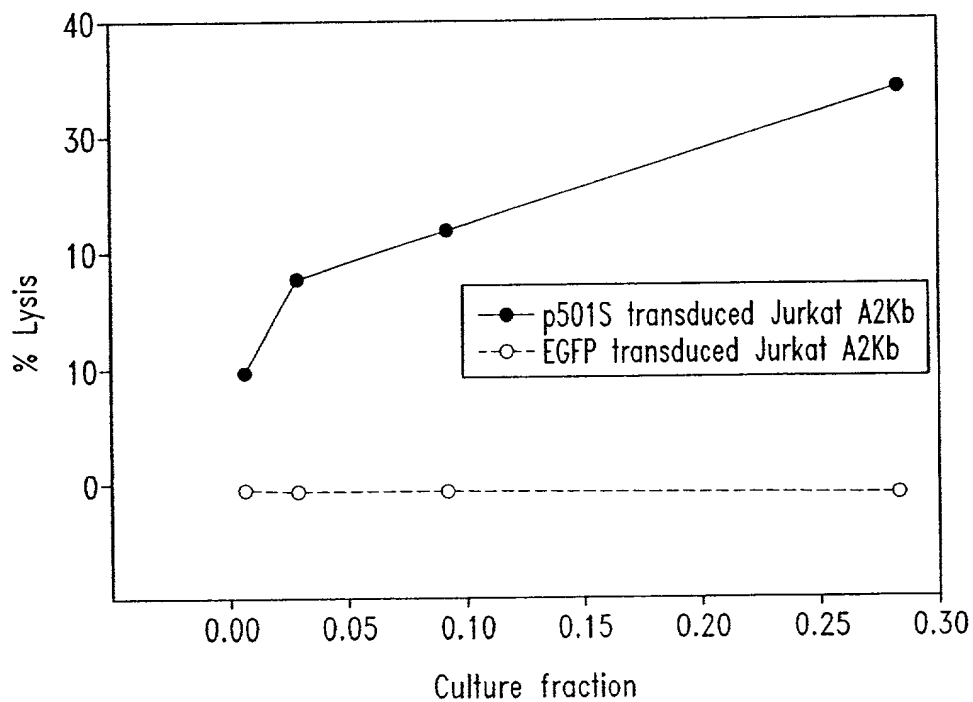


Fig. 5

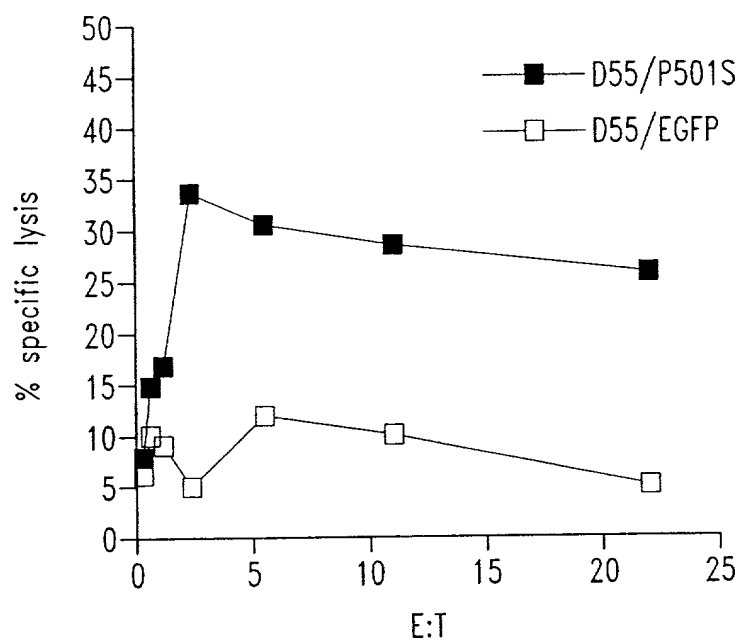


Fig. 6A

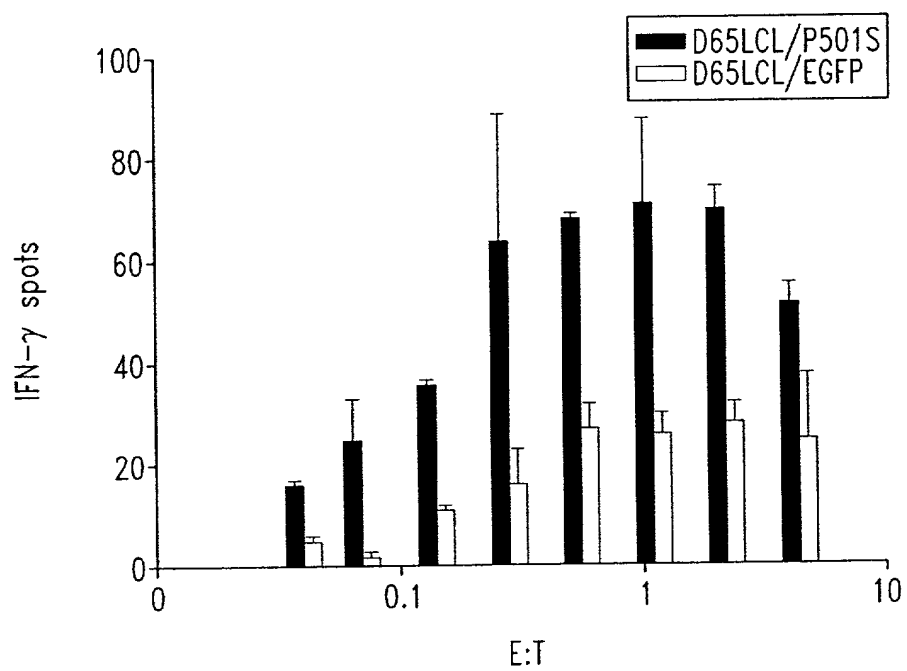
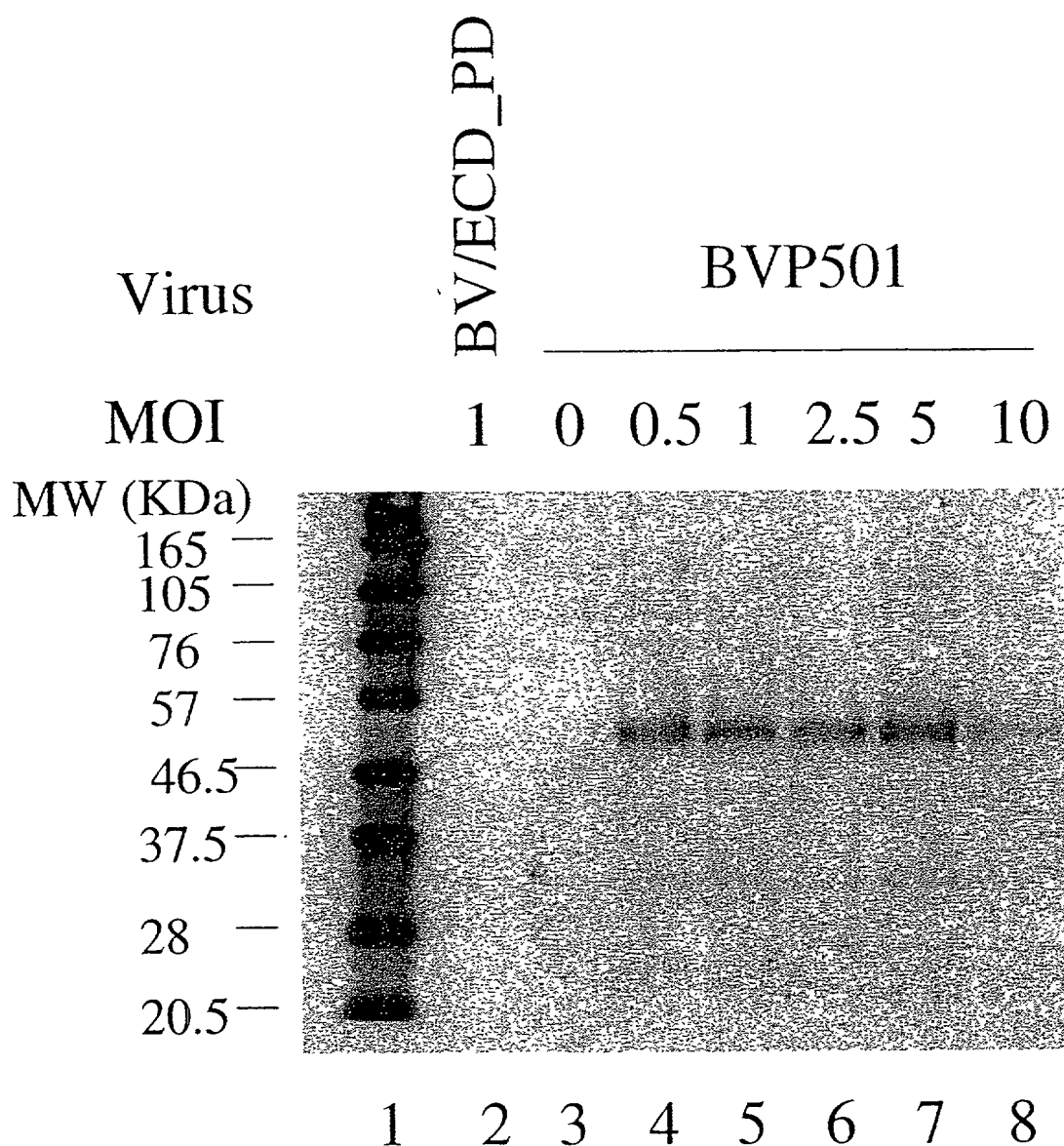


Fig. 6B

Expression of P501S by the Baculovirus Expression System



0.6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD_PD (lane 2), without virus (lane 3), or with recombinant baculovirus for P501 at different MOIs (lane 4 – 8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E3-G4D3). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

Fig. 7

Figure 8. Mapping of the epitope recognized by 10E3-G4-D3

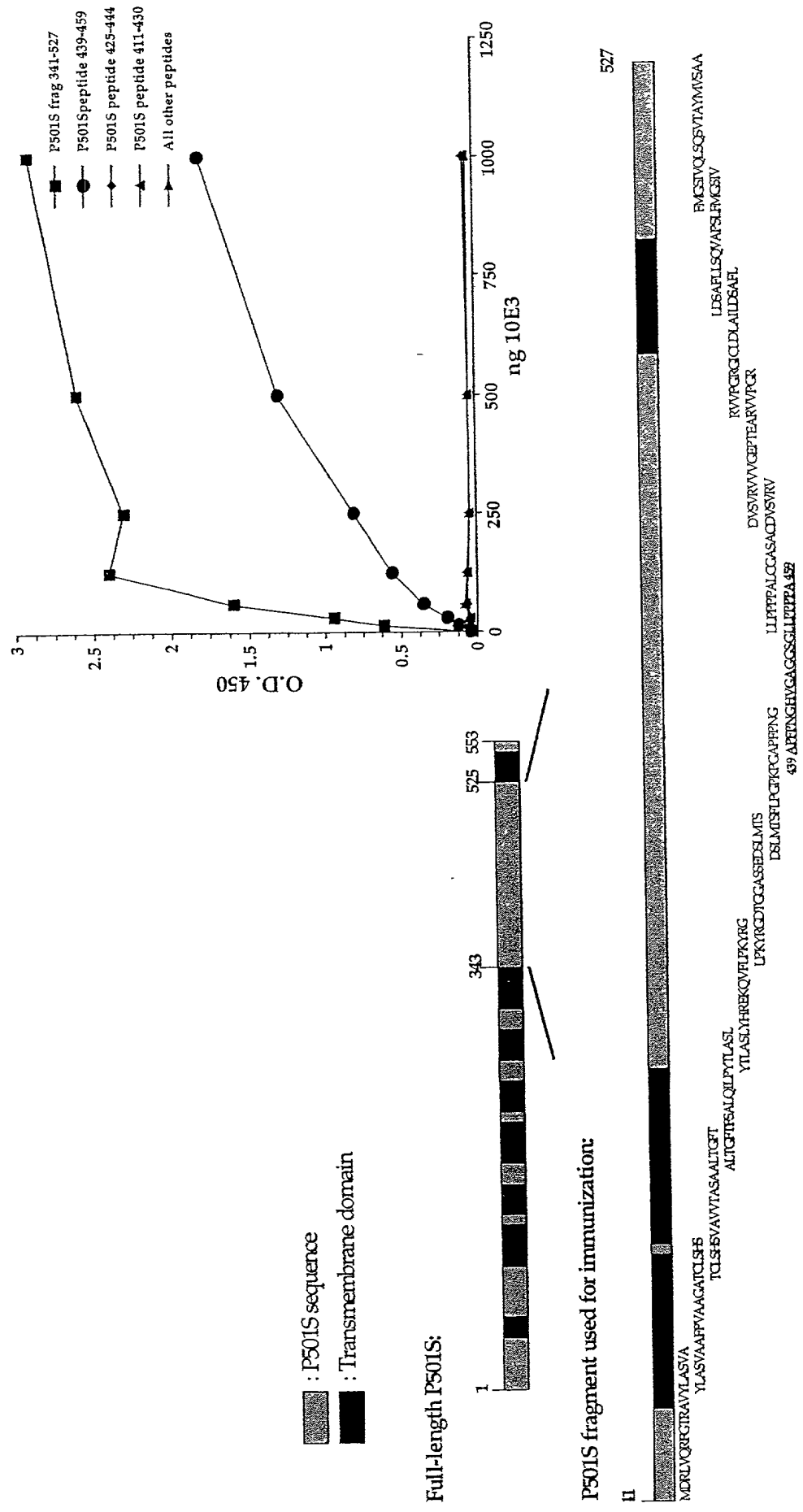


Fig. 8

7

Figure 1. Schematic of P501S with predicted transmembrane, cytoplasmic, and extracellular regions

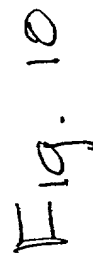
AMQDAWVYHLLRRK AQLHLYNLLTPGLFVCI AAGHT YVPM LLEVCVERIKFM TRIVLGIQPYLGLVCYPILEGSAE
 DWVRGRYRRRP EIWALSLGILLSEFLIPRAGWI AGH CPDPRPI E LALHLLGVCLLDFFCGQVCFITPL
 PALLSLFRDPDHCQ AYSYVAFHSLGGCTGYLIPAI DWDTSATAPVLCETQEE
 CLPGLLTLPLFCVNAATLY APTVAQPTLPVGLSAPSSPTGCPGRARAFRNIGAILPRL
 HQLCGRAPRTTR LPVAFI CSYMAIATETLYTP YEGGLYQGLVPILAPGTLEARRHIYDEGYR
 MGSILGLFLGCASLVSILYN DRIVQREGTRAVY AS VAAIPYAAQATCLSHSYAYVTA SAA
 LTGHTSALQILPYTLASLY HREKQVFLPKYRGDTGCASSEDSIATSFIPGPKPGAPFPNGHIVGAGGSGL
 APPPPALCGASACDVSVRVVVEPTEARVVPKRG ELLDLNHLPSAFLLSQYAPSLR MGSIVQLSQS
 YTAVMVSAAGILGLVALYFAT QVVFDSIAKYSK

Underlined sequence: Predicted transmembrane domain; Bold sequence: Predicted extracellular domain;

italic sequence: Predicted intracellular domain. Sequence in bold/underlined, used to generate polyclonal rabbit serum

Localization of domains predicted using HMMTOP (C.E. Tusnady and I. Simon (1998) Principles

Governing Amino Acid Composition of Integral Membrane Proteins: Applications to topology Prediction.J.Mol Biol. 283, 489-506.



1051

FIGURE 4. Elisa assay of rabbit polyclonal antibody specificity

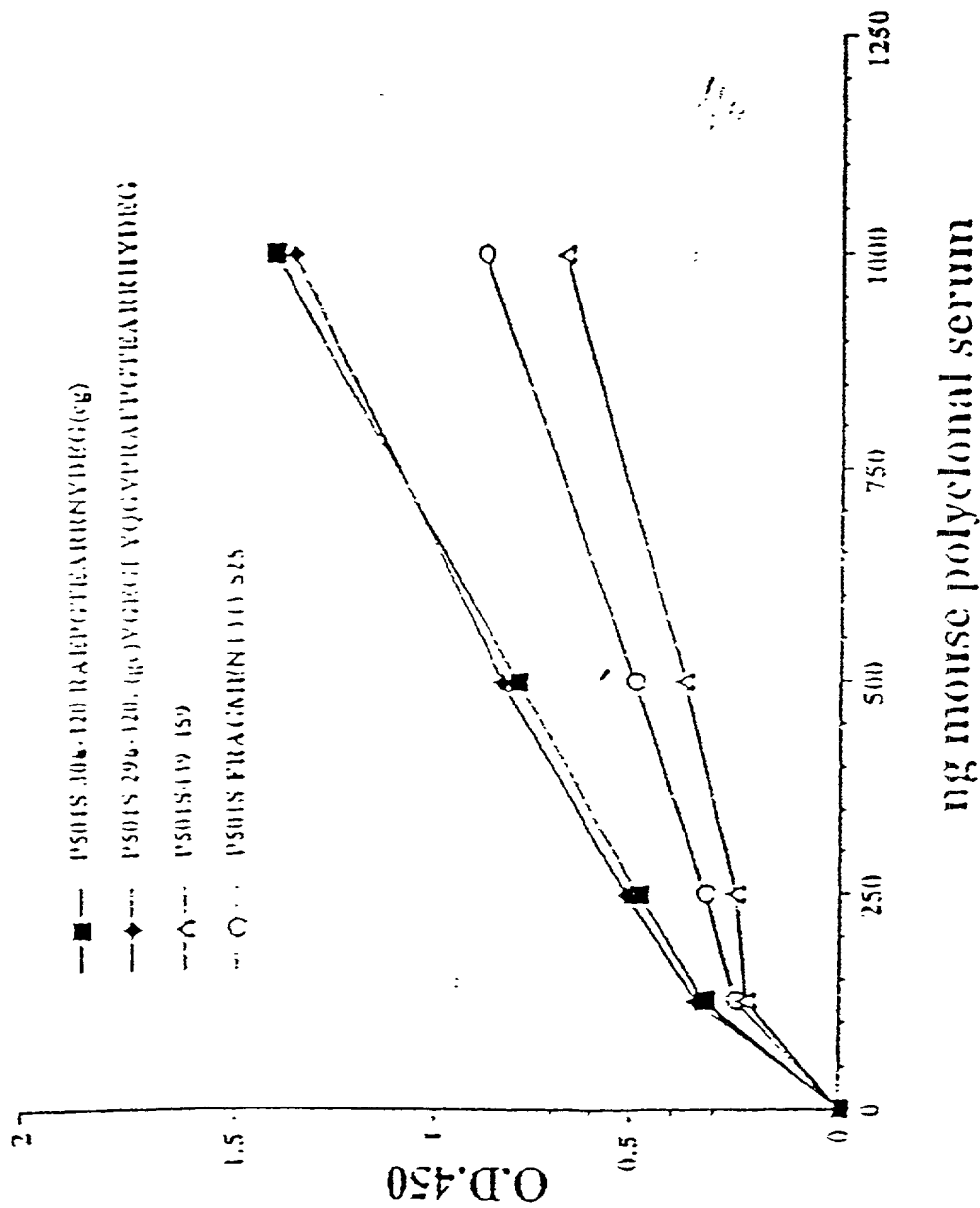


Fig. 11

10 20 30 40 50 60 70
 GTCACCTTAGGAAAAGGTGTCTTTTCGGGCAGCCGGGCTCAGCATGAGGAACAGAAGGAATGACACTCTGG 70
 ACAGCACCCCGGACCCTGTACTCCAGCGCGTCTCAGAGCACASACTTGTCTTACACTGAAAGCGACTTGGT 140
 GAATTTTATTCAGCAAATTTTAAGAAACGAGAATGTGTCTTCTTTACCAAAGATTCCAAGGCCACGGAG 210
 AATGTGTGCAAGTGTGGCTATGCCCAGAGCCAGCAGATGGAAGGCACCCAGATCAACCAAAGTGAGAAAT 280
 GGAAGTACAAGAAACACACCAAGGAATTTCTCTAGCCAGCGCTTTGGGGATATTTCAGTTTGAGACACTGGG 350
 360 370 380 390 400 410 420
 GAAGAAAGGGAAGTATATACGTCTGTCTTGCAGACAGGAGCGGAAATCTTTACGAGCTGCTGACCCAG 420
 CACTGGCACTTGAAAACAACCAACTGGTCAATTTCTGTACCGGGGGCGCCAAGAACTTCGCCCTGAAGC 490
 CGCGCATGCGCAAGATCTTCAGCCGGGCTCATCTACATCGCGCAGTCCAAAGGTGCTTGGATTCTCACGGG 560
 AGGCACCCATTATGGCCTGACGAAAGTACATCGGGGAGGTGGTGAGAGATAACACCATCAGCAGGAGTTCA 630
 GAGGAGAATATTGTGGCCATTGGCATAGCAGCTTGGGGCATGGTCTGAAACCGGGACACCCCTCATCAGGA 700
 710 720 730 740 750 760 770
 ATGGGATGCTGAGGGCTATTTTTTAGCCCACTACCTTATGGATGACTCACAAGGGATCCACTGTATAT 770
 GCTGGACAACAACACACACATTTGGTGTCTGGTGGAAATGGCTGTATGGACATCCCACTGTGGAAGCA 840
 AAGCTCCGGGAATCAGCTAGAGAAGCATATCTGTGAGCGCACTATTCAGATTCCAACTATGGTGGCAAGA 910
 TGGCCATTGTGTGTCTTGGCCAAAGGAGGTGGAAAGAGACTTGAAGGCCATCAATAGCTCCATCAAAAA 980
 TAAAAATTCCTTGTGTGGTGGTGGAAAGGCTCGGGCGGGATCGCTGATGTGATCGCTAGCCCTGGTGGAGGT 1050
 1060 1070 1080 1090 1100 1110 1120
 GAGGATGCCCCGACATCTTTCTCCCGTCAAGGAGAAGTGGTGGCTTTTTTACCCCGCACGGTGTCTCGGC 1120
 TGTCTGAGGAGGAGACTGAGAGTGGATCAAATGGCTCAAGAGAAATCTCGAATGTTCTCACCTATTAA 1190
 AGTTATTAAATGGAAAGAAAGTGGGGATGAAATGTGAGCAATGCCATCTCTACGGTCTATACAAAGCC 1260
 TCAGCACCGAGTGAGCAAGACAAAGGATAACTGGAAATGGGCCTGGAAGCTCTCTGGAGTGGAAACAGC 1330
 TGGAGTTAGCCCAATGATGAGATTTCACCAATGACCGCGGATGGGAGTCTGCTGACCTCAAGAAATCAT 1400
 1410 1420 1430 1440 1450 1460 1470
 GTTTACGGCTCTCATAAAGGACAGACCCAAAGTTGTCTCCCTCTTTCTGGAGAATGGCTTGAACCTACGG 1470
 AAGTTTCTCACCCATGATGTCTCACTGAAGCTCTCTCCAAAGCACTTCAGCACGCTTGTGTACCGGAATC 1540
 TGCAGATCGCCAAGAATTCCTATAATGATGCCCTCTCTACGCTTGTCTGGAACTGGTTGCCAACTTCCG 1610
 AAGAGGCTTCGGGAAGGAAGACAGAAATGGCGGGGATGAGATGGACATAGAATCCACGACGTGTCTCT 1680
 ATTACTCGGCAGCCCCCTGCAAGCTCTCTTCACTCGGGCATTTCTCAGAAAGGAAGGAATCTCTCAAAG 1750
 1760 1770 1780 1790 1800 1810 1820
 TCATTTGGGAGCAGACACAGGGGGCTGCACTCTGSCAGCCCTCGAGCCAGCAAGCTTCTGAAGACTCTGGC 1820
 CAAAGTGAAGACGACATCAATGCTGTGTGGGAGTTCGAGGAGCTGGCTAAAGAGTACGAGACCCCGGCT 1890
 GTTGAGCTGTCACTGAGTGTACAGGACCGATGAGAGACTTGGCAGAACAGCTGCTGGTCTATTCTGTG 1960
 AAGCTTGGGTGGAAAGCAACTGTCTGGAGCTGGGGTGGAGGCGAGAGACAGCATTTACCGGCCCAAGC 2030
 TGGGCTCCAGAAATTTCTTTCTAAGCAATGGTATGGAGAGATTTCGGAGACACCAAGAACTGGAGATT 2100

Fig. 12A (i)

2110	2120	2130	2140	2150	2160	2170
<p>TCCTGTGTCTGTTTATATACCCCTTGGTGGGCTGTGGCTTTGTATCATTTAGGAAGAAACCTGTGACA 2170</p> <p>AGCACAAGAAGCTGCTTTGGTACTATGTGGGCTCTTCACCTCCCGCTTCGTGGTCTTCTCCTGGAATGT 2240</p> <p>GGTCTTCTACATCGCCTTCTCTGCTGTTTCCCTACGTGCTGCTCATGGATTTCCATTTCGGTGCCACAC 2310</p> <p>CCCCCGAGCTGCTCCTGTACTCGCTGGTCTTTGTCCCTCTCTGTGATGAAGTCAGACAGTGGTACGTAA 2380</p> <p>ATGGGGTGAATTATTTTACTGACCTGTGGAATGTGATGGACACGCTGGGGCTTTTTTACTTCATAGCAGG 2450</p>						
2460	2470	2480	2490	2500	2510	2520
<p>AATTGTATTTGCGCTCCACTCTTCTAATAAAAGCTCTTTGTATCTCGGACGAGTCATTTCTGTCTGGAC 2520</p> <p>TACATTATTTTCACTCTAAGATTGATCCACATTTTACTGTAAGCAGAAACTTAGGACCCAAGATTATAA 2590</p> <p>TGCTGCAGAGGATGCTGATCGATGTGTCTCTCTCTGTTCTCTTTGCGGTGTGGATGGTGGCCTTTGG 2660</p> <p>CGTGGCCAGGCAAGGGATCTTAGGCAGATGAGCAGGCTGGAGGTGGATATTCCGTTGGGTCACTCTAC 2730</p> <p>GAGCCCTACCTGGCCATGTTCCGCCAGGTGCCAGTGACGTGGATGGTACCACGTATGACTTTGCCCACT 2800</p>						
2810	2820	2830	2840	2850	2860	2870
<p>GCACCTTCACTGGGAATGAGTCCAAGCCACTGTGTGTGGAGCTGATGAGCACAACCTGCCCGGTTCCC 2870</p> <p>CGAGTGGATCACCATCCCGCTGGTGTGCTCTACATGTTATCCACCAACATCCTGCTGGTCAACCTGCTG 2940</p> <p>GTCGCCATGTTTGGCTACACGGTGGGCACCGTCCAGGAGAACATGACCAAGGTCTGGAAGTTCCAGAGGT 3010</p> <p>ACTTCTTGTGTCAGGAGTATGTCAGGCGGCTCAATATCCCTTCCCTTCATGCTCTTGGCTTACTTCTA 3080</p> <p>CATGGTGTGTAAGAAGTCTTCAAGTGTGTGTGTAAGGAGAAACATGGAGTCTCTGTCTGCTGTTTC 3150</p>						
3160	3170	3180	3190	3200	3210	3220
<p>AAAAATGAAGACCAATGAGACTCTGGCATGGGAGGCTGCTCATGAAGGAAACCTACCTTGTCTAGATCACA 3220</p> <p>CAAAAGCCAAAGCAGACCTTCAGAGGAAATGAGGCACTGCAATTAGACCACTGGATACAAAGCTTAATGATCT 3290</p> <p>CAAGGGCTCTTCTGAAGAGATTGCTAATAAAATCAATTAAGCTGATGAAGCTCTAATGGAGAAAGATC 3360</p> <p>TAATTATAGCAAGATCATATTAAGGAATGCTGATGAACAAATTTGCTATCGACTACTAAATGASAGATTT 3430</p> <p>TCAGACCCCTGGGTACATGCTGGATGATTTAAATCACTTAGTGTGCTGAGACCTTGAGAATAAAGTGT 3500</p>						
3510	3520	3530	3540	3550	3560	3570
<p>CTGATTTGGTTTCATCTTGAAGACGGATATAAGGAGAAATATTTCTTTTATGTGTTCTCCAGAAATGGT 3570</p> <p>CGCTGTTTCTCTCTGTCTCTCAATGCCCTGGGACTGGAGGTGATAGTTTAAGTGTGTCTCTTACCGCCTCC 3640</p> <p>CTTTTCTCTTATCTTATTTTGGATGACACAATATAGGAGACATCTATCTATGAATAAGAACCTGG 3710</p> <p>CTCATGCTTACTCCTGTATTGTTATTTGTTCATTTCCAAATGATTCTCTACTTTTCCCTTTTGTATT 3780</p> <p>CATGTGACTAATAGTTGGCATAATGTAAAGTCTCTCAAAATAGGCCAGATTCTAAACATGCTGCAGC 3850</p>						
3860	3870	3880	3890	3900	3910	3920
<p>AAGAGGACCCCGCTCTCTTCAGGAAAGTGTTCATTTCTCAGGATGCTTCTTACCTGTGAGAGGAGGT 3920</p> <p>GACAAAGGCAGTCTCTGCTCTCTTGGACTCAGCAGGCTCTATTGAAGGAACCAACCCCATTCCTAAATA 3990</p> <p>TGTGAAAGGTGCCCCAAAATGCAACCTTGAAGGGCACTACTGACTTTGTTCTTATTGGATACTCCTTTA 4060</p> <p>TTTATTATTTTCCATTAAAAAATATAGCTGGCTATTATAGAAAATTTAGACCATACAGAGATGTAGAAA 4130</p> <p>GAACATAAATTGTCCCATTAACCTTAGGTAACTGCTAACAATTTCTGGATGGTTTTTCAAGTCTAT 4200</p>						
4210	4220	4230	4240	4250	4260	4270
<p>TTTTTTCTATATGATGCTCAATCTCTTTCAAAATTTACAGAAATGTTATCACTACATATATACTTT 4270</p> <p>TTATGTAAGCTTTTCACTTAGTATTTTATCAAAATATGTTTATATATTCATAGCTTCTTAACATT 4340</p> <p>ATATCAATTAATGCAATAATAGGCACCTCTAGGGATACCAATAATTTGCTCAATGAAGGCTATCTCCAG 4410</p> <p>TTGATCAATGGGATGAGCATCTGTGTGATGAATGCTATTTGGGAAATTTTCCAGGTTAG 4480</p> <p>ATTCCCAATAAATATCTATTTATTTAATATTAATATCAATATATTAATAAACCATTATTAAGCT 4550</p>						

Fig. 12A(2)

4560 4570 4580 4590 4600 4610 4620
 TTTTCATAAATGTATAGCAAAATAGGAATTATTAACCTTGAGCATAAGATATGAGATACATGAACCTGAACT 4620
 ATTAATAAATAAATATTATATTTAACCCTAGTTTAAGAAGAAGTCAATATGCTTATTTAAATATTATGGAT 4690
 GGTGGGCAGATCATTGAGGTCAGGAGTTCGAGACGAGCCTGGCCAACATGGCAAAACCACATCTCTACT 4760
 AAAAAATAAAAAAATAGCTGGGTGTGGTGGTGCACCTCTGTAATCCGAGCTACTCAGAAGGCTGAGGTAC 4830
 AAGAATTGCTGGAACCTGGGAGGCGGAGGTTGCAGTGAACCAAGATTGCACCACTGCACCTCCAGCCGGGG 4900
 4910 4920 4930 4940 4950 4960 4970
 TGACAGAGTGAGACTCCGACTGAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATATTATGG 4970
 ATGGTGAAGGGAATGGTATAGAATTGGAGAGATTATCTTACTGAACACCTGTAGTCCCAGCTTTCTCTGG 5040
 AAGTGGTGGTATTTGAGCAGGATGTGCACAAGGCAATTGAAATGCCATAATTAGTTTCTCAGCTTTGAA 5110
 TACACTATAAACTCAGTGGCTGAAGGAGGAAATTTTAGAAGGAAGCTACTAAAAGATCTAATTTGAAAAA 5180
 CTACAAAAGCATTAACATAAAAAAGTTTATTTCTCTTTGTCTGGGCAGTAGTGAAAATAAATACTACTCACA 5250
 5260 5270 5280 5290 5300 5310 5320
 CATTCACATATGTTTGAAGGAATTAACACAAATAAAAGATGCCTTTTACTTAAACGCCAAGACAGAAAA 5320
 CTTGCCCAATACTGAGAAGCAACTTGCATTAGAGAGGGAAGCTGTAAATGTTTTCAACCCAGTTTCATCTG 5390
 GTGGATGTTTTGACAGGTACTCTGAGAATTTTGCCTATGAAAAATCATTTATTTTAGTGTTAGTTTCAAA 5460
 TAATGTATTGAACATACTCTAATCAAGGCTGCTATGCTCTGTATGGTACTAAATGTGTCTCTGTGTAT 5530
 CTTTTGCACAACCTGAGAACTCTGCGGCTTGGTTTAAAGAGTGTGTTTCATGAAATAAATAATGGAGGAAT 5600
 5610 5620 5630 5640 5650 5660 5670
 GCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5668

Fig. 12A(3)

